

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FROMMER, Wolf-Bernd
- (ii) TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID  
TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS  
CONTAINING A TRANSPORTER AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
  - (B) STREET: 1180 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: NY
  - (E) COUNTRY: US
  - (F) ZIP: 10036-8403
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/362,512
  - (B) FILING DATE: 05-JAN-1995
  - (C) CLASSIFICATION: 800
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/007,636
  - (B) FILING DATE: 21-JAN-1993
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Meilman, Edward A.
  - (B) REGISTRATION NUMBER: 24,735
  - (C) REFERENCE/DOCKET NUMBER: P/951-107
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 382-0700
  - (B) TELEFAX: (212) 382-0888
  - (C) TELEX: 236925

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1685 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliano

05474-0540  
4445360

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..1511

(D) OTHER INFORMATION: /note= "amino acid transporter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTAAAACAT TTATTTTATC TTCTTCTTGT TCTCTCTTTC TCTTTCTCTC ATCACT	56
ATG AAG AGT TTC AAC ACA GAA GGA CAC AAC CAC TCC ACG GCG GAA TCC Met Lys Ser Phe Asn Thr Glu Gly His Asn His Ser Thr Ala Glu Ser	104
1 5 10 15	
GGC GAT GCC TAC ACC GTG TCG GAC CCG ACA AAG AAC GTC GAT GAA GAT Gly Asp Ala Tyr Thr Val Ser Asp Pro Thr Lys Asn Val Asp Glu Asp	152
20 25 30	
GGT CGA GAG AAG CGT ACC GGG ACG TGG CTT ACG GCG AGT GCG CAT ATT Gly Arg Glu Lys Arg Thr Gly Thr Trp Leu Thr Ala Ser Ala His Ile	200
35 40 45	
ATC ACG GCG GTG ATA GGC TCC GGA GTG TTG TCT TTA GCA TGG GCT ATA Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile	248
50 55 60	
GCT CAG CTT GGT TGG ATC GCA GGG ACA TCG ATC TTA CTC ATT TTC TCG Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile Leu Leu Ile Phe Ser	296
65 70 75 80	
TTC ATT ACT TAC TTC ACC TCC ACC ATG CTT GCC GAT TGC TAC CGT GCG Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ala	344
85 90 95	
CCG GAT CCC GTC ACC GGA AAA CGG AAT TAC ACT TAC ATG GAC GTT GTT Pro Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val	392
100 105 110	
CGA TCT TAC CTC GGT GGT AGG AAA GTG CAG CTC TGT GGA GTG GCA CAA Arg Ser Tyr Leu Gly Gly Arg Lys Val Gln Leu Cys Gly Val Ala Gln	440
115 120 125	
TAT GGG AAT CTG ATT GGG GTC ACT GTT GGT TAC ACC ATC ACT GCT TCT Tyr Gly Asn Leu Ile Gly Val Thr Val Gly Tyr Thr Ile Thr Ala Ser	488
130 135 140	
ATT AGT TTG GTA GCG GTA GGG AAA TCG AAC TGC TTC CAC GAT AAA GGG Ile Ser Leu Val Ala Val Gly Lys Ser Asn Cys Phe His Asp Lys Gly	536
145 150 155 160	
CAC ACT GCG GAT TGT ACT ATA TCG AAT TAT CCG TAT ATG GCG GTT TTT His Thr Ala Asp Cys Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe	584
165 170 175	
GGT ATC ATT CAA GTT ATT CTT AGC CAG ATC CCA AAT TTC CAC AAG CTC Gly Ile Ile Gln Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu	632
180 185 190	
TCT TTT CTT TCC ATT ATG GCC GCA GTC ATG TCC TTT ACT TAT GCA ACT Ser Phe Leu Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr	680

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195	200	205	
ATT GGA ATC GGT CTA GCC ATC GCA ACC GTC GCA GGT GGG AAA GTG GGT Ile Gly Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Gly Lys Val Gly 210 215 220			728
AAG ACG AGT ATG ACG GGC ACA GCG GTT GGA GTA GAT GTA ACC GCA GCT Lys Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala 225 230 235 240			776
CAA AAG ATA TGG AGA TCG TTT CAA GCG GTT GGG GAC ATA GCG TTC GCC Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe Ala 245 250 255			824
TAT GCT TAT GCC ACG GTT CTC ATC GAG ATT CAG GAT ACA CTA AGA TCT Tyr Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Arg Ser 260 265 270			872
AGC CCA GCT GAG AAC AAA GCC ATG AAA AGA GCA AGT CTT GTG GGA GTA Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val 275 280 285			920
TCA ACC ACC ACT TTT TTC TAC ATC TTA TGT GGA TGC ATC GGC TAT GCT Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys Ile Gly Tyr Ala 290 295 300			968
GCA TTT GGA AAC AAT GCC CCT GGA GAT TTC CTC ACA GAT TTC GGG TTT Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu Thr Asp Phe Gly Phe 305 310 315 320			1016
TTC GAG CCC TTT TGG CTC ATT GAC TTT GCA AAC GCT TGC ATC GCT GTC Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Ala Val 325 330 335			1064
CAC CTT ATT GGT GCC TAT CAG GTG TTC GCG CAG CCG ATA TTC CAG TTT His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe 340 345 350			1112
GAT GAG AAA AAA TGC AAC AGA AAC TAT CCA GAC AAC AAG TTC ATC ACT Val Glu Lys Lys Cys Asn Arg Asn Tyr Pro Asp Asn Lys Phe Ile Thr 355 360 365			1160
TCT GAA TAT TCA GTA AAC GTA CCT TTC CTT GGA AAA TTC AAC ATT AGC Ser Glu Tyr Ser Val Asn Val Pro Phe Leu Gly Lys Phe Asn Ile Ser 370 375 380			1208
CTC TTC AGA TTG GTG TGG AGG ACA GCT TAT GTG GTT ATA ACC ACT GTT Leu Phe Arg Leu Val Trp Arg Thr Ala Tyr Val Val Ile Thr Thr Val 385 390 395 400			1256
GTA GCT ATG ATA TTC CCT TTC TTC AAC GCG ATC TTA GGT CTT ATC GGA Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly 405 410 415			1304
GCA GCT TCC TTC TGG CCT TTA ACG GTT TAT TTC CCT GTG GAG ATG CAC Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His 420 425 430			1352
ATT GCA CAA ACC AAG ATT AAG AAG TAC TCT GCT AGA TGG ATT GCG CTG Ile Ala Gln Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu			1400



145		150		155		160
His Thr Ala Asp Cys Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe						
		165		170		175
Gly Ile Ile Gln Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu						
		180		185		190
Ser Phe Leu Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr						
		195		200		205
Ile Gly Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Gly Lys Val Gly						
		210		215		220
Lys Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala						
		225		230		235
Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe Ala						
		245		250		255
r Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Arg Ser						
		260		265		270
Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val						
		275		280		285
Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys Ile Gly Tyr Ala						
		290		295		300
Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu Thr Asp Phe Gly Phe						
		305		310		315
Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Ala Val						
		325		330		335
His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe						
		340		345		350
Val Glu Lys Lys Cys Asn Arg Asn Tyr Pro Asp Asn Lys Phe Ile Thr						
		355		360		365
Ser Glu Tyr Ser Val Asn Val Pro Phe Leu Gly Lys Phe Asn Ile Ser						
		370		375		380
Leu Phe Arg Leu Val Trp Arg Thr Ala Tyr Val Val Ile Thr Thr Val						
		385		390		395
Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly						
		405		410		415
Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His						
		420		425		430
Ile Ala Gln Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu						
		435		440		445
Lys Thr Met Cys Tyr Val Cys Leu Ile Val Ser Leu Leu Ala Ala Ala						
		450		455		460
Gly Ser Ile Ala Gly Leu Ile Ser Ser Val Lys Thr Tyr Lys Pro Phe						

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480

	Ser	Phe	Ile	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Glu	Leu	Val	Ala	Pro
	Ala	Val	Ser	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Glu	Leu	Val	Ala	Pro
			110					115					120				

Variable	Unit	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																						
Population	millions	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4	31.5	31.6	31.7	31.8	31.9	32.0	32.1	32.2	32.3	32.4	32.5	32.6	32.7	32.8	32.9	33.0	33.1	33.2	33.3	33.4	33.5	33.6	33.7	33.8	33.9	34.0	34.1	34.2	34.3	34.4	34.5	34.6	34.7	34.8	34.9	35.0	35.1	35.2	35.3	35.4	35.5	35.6	35.7	35.8	35.9	36.0	36.1	36.2	36.3	36.4	36.5	36.6	36.7	36.8	36.9	37.0	37.1	37.2	37.3	37.4	37.5	37.6	37.7	37.8	37.9	38.0	38.1	38.2	38.3	38.4	38.5	38.6	38.7	38.8	38.9	39.0	39.1	39.2

ATT Ile	CTC Leu	GGT Gly	GGG Gly	TTC Phe	AAG Lys	TC Phe	AAG Lys	ATT Ile	TGT Cys	GGG Gly	TTG Leu	ATC Ile	JAA Gln	TAC Tyr	TTG Leu	496
125						130					135					
AAT Asn	CTC Leu	TTT Phe	GGT Gly	ATC Ile	GCA Ala	ATT Ile	GGA Gly	TAC Tyr	ACG Thr	ATA Ile	GCA Ala	GCT Ala	TCC Ser	ATA Ile	AGC Ser	544
140					145					150					155	
ATG Met	ATG Met	GCG Ala	ATC Ile	AAG Lys	AGA Arg	TCC Ser	AAC Asn	TGC Cys	TTC Phe	CAC His	AAG Lys	AGT Ser	GGA Gly	GGA Gly	AAA Lys	592
				160					165					170		
GAC Asp	CCA Pro	TGT Cys	CAC His	ATG Met	TCC Ser	AGT Ser	AAT Asn	CCT Pro	TAC Tyr	ATG Met	ATC Ile	GTA Val	TTT Phe	GGT Gly	GTG Val	640
			175					180					185			
GCA Ala	GAG Glu	ATC Ile	TTG Leu	CTC Leu	TCT Ser	CAG Gln	GTT Val	CCT Pro	GAT Asp	TTC Phe	GAT Asp	CAG Gln	ATT Ile	TGG Trp	TGG Trp	688
			190				195					200				
TCC Ser	ATT Ile	GTT Val	GCA Ala	GCT Ala	GTT Val	ATG Met	TCC Ser	TTC Phe	ACT Thr	TAC Tyr	TCT Ser	GCC Ala	ATT Ile	GGT Gly		736
205					210					215						
CTA Leu	GCT Ala	CTT Leu	GGA Gly	ATC Ile	GTT Val	CAA Gln	GTT Val	GCA Ala	GCG Ala	AAT Asn	GGA Gly	GTT Val	TTC Phe	AAA Lys	GGA Gly	784
220					225					230					235	
AGT Ser	CTC Leu	ACT Thr	GGA Gly	ATA Ile	AGC Ser	ATC Ile	GGA Gly	ACA Thr	GTG Val	ACT Thr	CAA Gln	ACA Thr	CAG Gln	AAG Lys	ATA Ile	832
				240					245					250		
TGG Trp	AGA Arg	ACC Thr	TTC Phe	CAA Gln	GCA Ala	CTT Leu	GGA Gly	GAC Asp	ATT Ile	GCC Ala	TTT Phe	GCG Ala	TAC Tyr	TCA Ser	TAC Tyr	880
			255					260					265			
TCT Trp	GTT Val	GTC Val	CTA Leu	ATC Ile	GAG Glu	ATT Ile	CAG Gln	GAT Asp	ACT Thr	GTA Val	AGA Arg	TCC Ser	CCA Pro	CCG Pro	GCG Ala	928
			270				275					280				
GAA Glu	TCG Ser	AAA Lys	ACG Thr	ATG Met	AAG Lys	AAA Lys	GCA Ala	ACA Thr	AAA Lys	ATC Ile	AGT Ser	ATT Ile	GCC Ala	GTC Val	ACA Thr	976
			285			290					295					
ACT Thr	ATC Ile	TTC Phe	TAC Tyr	ATG Met	CTA Leu	TGT Cys	GGC Gly	TCA Ser	ATG Met	GGT Gly	TAT Tyr	GCC Ala	GCT Ala	TTT Phe	GGA Gly	1024
300					305					310					315	
GAT Asp	GCA Ala	GCA Ala	CCG Pro	GGA Gly	AAC Asn	CTC Leu	CTC Leu	ACC Thr	GGT Gly	TTT Phe	GGA Gly	TTC Phe	TAC Tyr	AAC Asn	CCG Pro	1072
				320					325					330		
TTT Phe	TGG Trp	CTC Leu	CTT Leu	GAC Asp	ATA Ile	GCT Ala	AAC Asn	GCC Ala	GCC Ala	ATT Ile	GTT Val	GTC Val	CAC His	CTC Leu	GTT Val	1120
			335					340					345			
GGA Gly	GCT Ala	TAC Tyr	CAA Gln	GTC Val	TTT Phe	GCT Ala	CAG Gln	CCC Pro	ATC Ile	TTT Phe	GCC Ala	TTT Phe	ATT Ile	GAA Glu	AAA Lys	1168
		350					355					360				

TCA GTC GCA GAG AGA TAT C A GAC AAT GAC TTC CTC AGC AG GAA TTT Ser Val Ala Glu Arg Tyr Pro Asp Asn Asp Phe Leu Ser Lys Glu Phe 365 370 375	1216
GAA ATC AGA ATC CCC GGA TTT AAG TCT CCT TAC AAA GTA AAC GTT TTC Glu Ile Arg Ile Pro Gly Phe Lys Ser Pro Tyr Lys Val Asn Val Phe 380 385 390 395	1264
AGG ATG GTT TAC AGG AGT GGC TTT GTC GTT ACA ACC ACC GTG ATA TCG Arg Met Val Tyr Arg Ser Gly Phe Val Val Thr Thr Thr Val Ile Ser 400 405 410	1312
ATG CTG ATG CCG TTT TTT AAC GAC GTG GTC GGG ATC TTA GGG GCG TTA Met Leu Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Leu 415 420 425	1360
GGG TTT TGG CCC TTG ACG GTT TAT TTT CCG GTG GAG ATG TAT ATT AAG Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Lys 430 435 440	1408
C C AGG AAG GTT GAG AAA TGG AGC ACG AGA TGG GTG TGT TTA CAG ATG C A Arg Lys Val Glu Lys Trp Ser Thr Arg Trp Val Cys Leu Gln Met 445 450 455	1456
CTT AGT GTT GCT TGT CTT GTG ATC TCG GTG GTC GCC GGG GTT GGA TCA Leu Ser Val Ala Cys Leu Val Ile Ser Val Val Ala Gly Val Gly Ser 460 465 470 475	1504
ATC GCC GGA GTG ATG CTT GAT CTT AAG GTC TAT AAG CCA TTC AAG TCT Ile Ala Gly Val Met Leu Asp Leu Lys Val Tyr Lys Pro Phe Lys Ser 480 485 490	1552
ACA TAT TGATGATTAT GGACCATGAA CAACAGAGAG AGTTGGTGTG TAAAGTTTAC Thr Tyr	1608
CATTTCAAAG AAAACTCCAA AAATGTGTAT ATTGTATGTT GTTCTCATTT CGTATGGTCT	1668
CATCTTTGTA ATAAAATTTA AAACCTATGT TATAAATTAT AAAAAAAAAA AAAAAAAAAA	1728
AAAAAAAAAA AA	1740

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Glu	Thr	Ala	Ala	Ala	Asn	Asn	His	Arg	His	His	His	His	His
1				5					10					15	
Gly	His	Gln	Val	Phe	Asp	Val	Ala	Ser	His	Asp	Phe	Val	Pro	Pro	Gln
			20					25					30		



Pro Ala Phe Lys Cys Phe . .p Asp Asp Gly Arg Leu Lys .rg Thr Gly  
 35 40 45  
 Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser  
 50 55 60  
 Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala  
 65 70 75 80  
 Gly Pro Ala Val Met Leu Leu Phe Ser Leu Val Thr Leu Tyr Ser Ser  
 85 90 95  
 Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp Ala Val Ser Gly Lys  
 100 105 110  
 Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser Ile Leu Gly Gly Phe  
 115 120 125  
 Lys Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile  
 130 135 140  
 . . Ile Gly Tyr Thr Ile Ala Ala Ser Ile Ser Met Met Ala Ile Lys  
 145 150 155 160  
 Arg Ser Asn Cys Phe His Lys Ser Gly Gly Lys Asp Pro Cys His Met  
 165 170 175  
 Ser Ser Asn Pro Tyr Met Ile Val Phe Gly Val Ala Glu Ile Leu Leu  
 180 185 190  
 Ser Gln Val Pro Asp Phe Asp Gln Ile Trp Trp Ile Ser Ile Val Ala  
 195 200 205  
 Ala Val Met Ser Phe Thr Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile  
 210 215 220  
 Val Gln Val Ala Ala Asn Gly Val Phe Lys Gly Ser Leu Thr Gly Ile  
 5 230 235 240  
 Ser Ile Gly Thr Val Thr Gln Thr Gln Lys Ile Trp Arg Thr Phe Gln  
 245 250 255  
 Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Val Val Leu Ile  
 260 265 270  
 Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala Glu Ser Lys Thr Met  
 275 280 285  
 Lys Lys Ala Thr Lys Ile Ser Ile Ala Val Thr Thr Ile Phe Tyr Met  
 290 295 300  
 Leu Cys Gly Ser Met Gly Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly  
 305 310 315 320  
 Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn Pro Phe Trp Leu Leu Asp  
 325 330 335  
 Ile Ala Asn Ala Ala Ile Val Val His Leu Val Gly Ala Tyr Gln Val  
 340 345 350

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